

SEQUENCE LISTING

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 KITAMURA, TOSHIO

<120> METHOD FOR SCREENING CANDIDATE COMPOUNDS FOR ANTITUMOR DRUG

<130> 084335/0129

<140>

<141>

<150> PCT/JP99/04450

<151> 1999-08-19

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<151> 1998-08-20

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 319

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(318)

<223> FLT3/ITD gene (Mt1); partial sequence

<400> 1

caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc	48
Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser	
1 5 10 15	
tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa tat gat	96
Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp	
20 25 30	
ctc aaa tgg gag ttt cca aga gaa aat tgc tcc tca gat aat gag tac	144
Leu Lys Trp Glu Phe Pro Arg Glu Asn Cys Ser Ser Asp Asn Glu Tyr	
35 40 45	
ttc tac gtt gat ttc aga gaa tat gaa tat gat ctc aaa tgg gag ttt	192
Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe	
50 55 60	
cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt	240
Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe	
65 70 75 80	

gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc 288
 Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
 85 90 95

tca atc cag gtt gcc gtc aaa atg ctg aaa g 319
 Ser Ile Gln Val Ala Val Lys Met Leu Lys
 100 105

<210> 2
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <223> FLT3/ITD (Mt1); partial sequence
 ITD region (42)..(68)

<400> 2
 Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
 1 5 10 15
 Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
 20 25 30
 Leu Lys Trp Glu Phe Pro Arg Glu Asn Cys Ser Ser Asp Asn Glu Tyr
 35 40 45
 Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
 50 55 60
 Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
 65 70 75 80
 Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
 85 90 95
 Ser Ile Gln Val Ala Val Lys Met Leu Lys
 100 105

<210> 3
 <211> 298
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(297)
 <223> FLT3/ITD gene (Mt2); partial sequence

<400> 3
 caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc 48
 Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
 1 5 10 15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa tat gat 96
 Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
 20 25 30

ctc aaa agc tcc tca gat aat gag tac ttc tac gtt gat ttc aga gaa 144
 Leu Lys Ser Ser Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu
 35 40 45

tat gaa tat gat ctc aaa tgg gag ttt cca aga gaa aat tta gag ttt 192
 Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe
 50 55 60

ggg aag gta cta gga tca ggt gct ttt gga aaa gtg atg aac gca aca 240
 Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val Met Asn Ala Thr
 65 70 75 80

gct tat gga att agc aaa aca gga gtc tca atc cag gtt gcc gtc aaa 288
 Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys
 85 90 95

atg ctg aaa g 298
 Met Leu Lys

<210> 4
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <223> FLT3/ITD (Mt2); partial sequence
 ITD region (35)..(54)

<400> 4
 Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
 1 5 10 15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp
 20 25 30

Leu Lys Ser Ser Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu
 35 40 45

Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe
 50 55 60

Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val Met Asn Ala Thr
 65 70 75 80

Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys
 85 90 95

Met Leu Lys

<210> 5
 <211> 271

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(270)

<223> FLT3/ITD gene (Mt3); partial sequence

<400> 5

caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc 48
Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
1 5 10 15

tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gaa atg gga 96
Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Met Gly
20 25 30

atg ggg gga gaa tgt aat ccc ggg aga caa gat ctc aaa tgg gag ttt 144
Met Gly Gly Glu Cys Asn Pro Gly Arg Gln Asp Leu Lys Trp Glu Phe
35 40 45

cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt 192
Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
50 55 60

gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc 240
Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
65 70 75 80

tca atc cag gtt gcc gtc aaa atg ctg aaa g 271
Ser Ile Gln Val Ala Val Lys Met Leu Lys
85 90

<210> 6

<211> 90

<212> PRT

<213> Homo sapiens

<220>

<223> FLT3/ITD (Mt3); partial sequence
ITD region (31)..(42)

<400> 6

Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
1 5 10 15

Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Glu Met Gly
20 25 30

Met Gly Gly Glu Cys Asn Pro Gly Arg Gln Asp Leu Lys Trp Glu Phe
35 40 45

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
50 55 60

Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
65 70 75 80

Ser Ile Gln Val Ala Val Lys Met Leu Lys
 85 90

<210> 7
 <211> 271
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(270)
 <223> FLT3/ITD gene (Mt4); partial sequence

<400> 7
 caa ttt agg tat gaa agc cag cta cag atg gta cag gtg acc ggc tcc 48
 Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
 1 5 10 15
 tca gat aat gag tac ttc tac gtt gat ttc aga gaa tat gat gag tac 96
 Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Asp Glu Tyr
 20 25 30
 ttc tac gtt gat ttc aga gaa tat gaa tat gat ctc aaa tgg gag ttt 144
 Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
 35 40 45
 cca aga gaa aat tta gag ttt ggg aag gta cta gga tca ggt gct ttt 192
 Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
 50 55 60
 gga aaa gtg atg aac gca aca gct tat gga att agc aaa aca gga gtc 240
 Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
 65 70 75 80
 tca atc cag gtt gcc gtc aaa atg ctg aaa g 271
 Ser Ile Gln Val Ala Val Lys Met Leu Lys
 85 90

<210> 8
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <223> FLT3/ITD (Mt4); partial sequence
 ITD region (30)..(40)

<400> 8
 Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Val Gln Val Thr Gly Ser
 1 5 10 15
 Ser Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Glu Tyr Asp Glu Tyr
 20 25 30

Phe Tyr Val Asp Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe
 35 40 45

Pro Arg Glu Asn Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe
 50 55 60

Gly Lys Val Met Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val
 65 70 75 80

Ser Ile Gln Val Ala Val Lys Met Leu Lys
 85 90

<210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: A primer for
 amplifying human FLT3/ITD genes

<400> 9
 caacaattgg tgtttgtctc ctctt 25

<210> 10
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: A primer for
 amplifying human FLT3/ITD genes.

<400> 10
 catgatatct cgagccaatc caaag 25